

In the Specification

Please substitute the Title of the invention on page 1, beginning at line 1:

~~C1q-related protein~~ Isolated INSP163 Protein

Please substitute the following paragraph on page 25, beginning at line 17:

The functionally-equivalent polypeptides of the first aspect of the invention may be polypeptides that are homologous to the INSP163 polypeptides. Two polypeptides are said to be "homologous", as the term is used herein, if the sequence of one of the polypeptides has a high enough degree of identity or similarity to the sequence of the other polypeptide. "Identity" indicates that at any particular position in the aligned sequences, the amino acid residue is identical between the sequences. "Similarity" indicates that, at any particular position in the aligned sequences, the amino acid residue is of a similar type between the sequences. Degrees of identity and similarity can be readily calculated (Computational Molecular Biology, Lesk, A.M., ed., Oxford University Press, New York, 1988; Biocomputing. Informatics and Genome Projects, Smith, D.W., ed., Academic Press, New York, 1993; Computer Analysis of Sequence Data, Part 1, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). Percentage identity, as referred to herein, is as determined using BLAST version 2.1.3 using the default parameters specified by the NCBI (the National Center for Biotechnology Information; ~~http://www~~ See Worldwide Website: ncbi.nlm.nih.gov/) [Blosum 62 matrix; gap open penalty=11 and gap extension penalty=1].

Please substitute the following paragraph on page 59, beginning at line 26:

**Figure 2:** Nucleotide sequence (SEQ ID NO:49) with translation of the INSP163 PCR product (SEQ ID NO:30) cloned using primers INSP163-CP1 (SEQ ID NO:37) and INSP163-CP2 (SEQ ID NO:38). The c1q domain is boxed. The collagen domain is shaded. Position and sense of primers are indicated by arrows.

Please substitute the following paragraph on page 60, beginning at line 1:

**Figure 3**FIGURES 3A-3F: Polypeptide sequences of predicted biologically active products after proprotein cleavage (cleavage sites are indicated in table 1). A) INSP163-A (SEQ ID NO:4), B) INSP163-B (SEQ ID NO:6), C) INSP163-C (SEQ ID NO:8), D) INSP163-D (SEQ ID NO:10), E) INSP163-E (SEQ ID NO:12) and F) INSP163-F (SEQ ID NO:14).

Please substitute the following Table 2 on page 66:

Table 2: INSP163 cloning and sequencing primers

Primer	Sequence (5'-3')
INSP163-CP1	TGA GCC GCC TCG GGA CGG AGC CAT ( <u>SEQ ID NO:37</u> )
INSP163-CP2	ACG TGC CCA GGA GCA GCC CGG AGA ( <u>SEQ ID NO:38</u> )
INSP163-EX1	GCA GGC TTC <u>GCC ACC</u> ATG CGG CGC TGG GCC TGG GC ( <u>SEQ ID NO:39</u> )
INSP163-EX2	<u>TG ATG GTG ATG GTG</u> CGT GCC CAG GAG CAG CCC GGA ( <u>SEQ ID NO:40</u> )
GCP Forward	G GGG ACA AGT TTG TAC AAA AAA GCA GGC TTC <u>GCC ACC</u> ( <u>SEQ ID NO:41</u> )
GCP Reverse	GGG GAC CAC TTT GTA CAA GAA AGC TGG GTT <b>TCA</b> <u>ATG GTG ATG GTG</u> ( <u>SEQ ID NO:42</u> )
pEAK12F	GCC AGC TTG GCA CTT GAT GT ( <u>SEQ ID NO:43</u> )
pEAK12R	GAT GGA GGT GGA CGT GTC AG ( <u>SEQ ID NO:44</u> )
21M13	TGT AAA ACG ACG GCC AGT ( <u>SEQ ID NO:45</u> )
M13REV	CAG GAA ACA GCT ATG ACC ( <u>SEQ ID NO:46</u> )
T7	TAA TAC GAC TCA CTA TAG G ( <u>SEQ ID NO:47</u> )
T3	ATT AAC CCT CAC TAA AGG ( <u>SEQ ID NO:48</u> )

Please substitute pages 1-25 (Sequence Listing) with the accompanying Sequence Listing (pages 1-27).